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IFWO

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/798,579DATE: 03/22/2004  
TIME: 10:19:03Input Set : A:\PTO.DA.txt  
Output Set: N:\CRF4\03222004\J798579.raw

2 <110> APPLICANT: Kirin Beer Kabushiki Kaisha; Japan International Research Center f  
3 cr Agricultural Sciences  
5 <120> TITLE OF INVENTION: A production of plants having improved rooting efficiency  
ind vase  
6 life by using environmental stress-resistant gene  
8 <130> FILE REFERENCE: PH-2034  
--> 10 <140> CURRENT APPLICATION NUMBER: US/10/798,579  
--> 10 <141> CURRENT FILING DATE: 2004-03-12  
10 <150> PRIOR APPLICATION NUMBER: JP 2003-071082  
11 <151> PRIOR FILING DATE: 2003-03-14  
13 <160> NUMBER OF SEQ ID NOS: 30

## ERRORED SEQUENCES

73 <210> SEQ ID NO: 2  
74 <211> LENGTH: 216  
75 <212> TYPE: PRT  
76 <213> ORGANISM: Arabidopsis thaliana  
78 <400> SEQUENCE: 2  
79 Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu.  
E--> 80 1 5 5 10 15 10 15  
81 Ser Ser Val Ser Ser Gly Gly Asp Tyr Ile Pro Thr Leu Ala Ser Ser  
E--> 82 20 20 25 30 25 30  
83 Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His  
E--> 84 35 35 40 40 45 45  
85 Pro Ile Tyr Arg Gly Val Arg Arg Arg Asn Ser Gly Lys Trp Val Cys  
E--> 86 50 55 50 60 60  
87 Glu Val Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe  
E--> 88 65 70 75 80  
89 Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala  
E--> 90 85 85 90 90 95 95  
91 Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg  
E--> 92 100 100 105 110 110 110  
93 Leu Arg Ile Pro Gly Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala  
E--> 94 115 115 120 120 125 125  
95 Ala Glu Ala Ala Leu Ala Phe Gln Asp Glu Met Cys Asp Ala Thr Thr  
E--> 96 120 130 135 135 140 140  
97 Asp His Gly Phe Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr Thr  
E--> 98 145 150 155 155 160 155 160 160  
99 Ala Glu Gln Ser Glu Asn Ala Phe Tyr Met His Asp Glu Ala Met Phe  
E--> 100 165 165 170 170 175 170 175 175  
101 Glu Met Pro Ser Leu Leu Ala Asn Met Ala Glu Gly Met Leu Leu Pro  
E--> 102 180 180 185 185 190 185 190 190

Please see item  
✓ # 3 & 4  
ON error (PS.1-15)  
summary sheet.  
Does Not Comply  
Corrected Diskette Needed

Input Set : A:\PTO.DA.txt  
Output Set: N:\CRF4\03222004\J798579.raw

103 Leu Pro Ser Val Gln Trp Asn His Asn His Glu Val Asp Gly Asp Asp  
--> 104 195 200 205

105 Asp Asp Val Ser Leu Trp Ser Tyr

--> 106 210 215

191 <210> SEQ ID NO: 4

192 <211> LENGTH: 335

193 <212> TYPE: PRT

194 <213> ORGANISM: Arabidopsis thaliana

196 <400> SEQUENCE: 4

197 Met Ala Val Tyr Asp Gln Ser Gly Asp Arg Asn Arg Thr Gln Ile Asp

--> 198 1 5 10 15

199 Thr Ser Arg Lys Arg Lys Ser Arg Gly Asp Gly Thr Thr Val

--> 200 20 25 30

201 Ala Glu Arg Leu Lys Arg Trp Lys Glu Tyr Asn Glu Thr Val Glu Glu

--> 202 35 40 45

203 Val Ser Thr Lys Lys Arg Lys Val Pro Ala Lys Gly Ser Lys Lys Gly

--> 204 50 55 60

205 Cys Met Lys Gly Lys Gly Pro Glu Asn Ser Arg Cys Ser Phe Arg

--> 206 65 70 75 80

207 Gly Val Arg Gln Arg Ile Trp Gly Lys Trp Val Ala Glu Ile Arg Glu

--> 208 85 90 95

209 Pro Asn Arg Gly Ser Arg Leu Trp Leu Gly Thr Phe Pro Thr Ala Gln

--> 210 100 105 110

211 Glu Ala Ala Ser Ala Tyr Asp Glu Ala Ala Lys Ala Met Tyr Gly Pro

--> 212 115 120 125

213 Leu Ala Arg Leu Asn Phe Pro Arg Ser Asp Ala Ser Glu Val Thr Ser

--> 214 130 135 140

215 Thr Ser Ser Gln Ser Glu Val Cys Thr Val Glu Thr Pro Gly Cys Val

--> 216 145 150 155 160

217 His Val Lys Thr Glu Asp Pro Asp Cys Glu Ser Lys Pro Phe Ser Gly

--> 218 165 170 175

219 Gly Val Glu Pro Met Tyr Cys Leu Glu Asn Gly Ala Glu Glu Met Lys

--> 220 180 185 190

221 Arg Gly Val Lys Ala Asp Lys His Trp Leu Ser Glu Phe Glu His Asn

--> 222 195 200 205

223 Tyr Trp Ser Asp Ile Leu Lys Glu Lys Gln Lys Glu Gln Gly

--> 224 210 215 220

225 Ile Val Glu Thr Cys Gln Gln Gln Asp Ser Leu Ser Val Ala

--> 226 225 230 235 240

227 Asp Tyr Gly Trp Pro Asn Asp Val Asp Gln Ser His Leu Asp Ser Ser

--> 228 245 250 255

229 Asp Met Phe Asp Val Asp Glu Leu Leu Arg Asp Leu Asn Gly Asp Asp

--> 230 260 265 270

231 Val Phe Ala Gly Leu Asn Gln Asp Arg Tyr Pro Gly Asn Ser Val Ala

--> 232 275 280 285

233 Asn Gly Ser Tyr Arg Pro Glu Ser Gln Gln Ser Gly Phe Asp Pro Leu

--> 234 290 295 300

235 Gln Ser Leu Asn Tyr Gly Ile Pro Pro Phe Gln Leu Glu Gly Lys Asp

--> 236 305 310 315 320

some errors

Input Set : A:\PTO.DA.txt  
Output Set: N:\CRF4\03222004\J798579.raw

237 Gly Asn Gly Phe Phe Asp Asp Leu Ser Tyr Leu Asp Ley Glu Asn  
--> 238        325        330        335        *Same errors*  
300 <210> SEQ ID NO: 6  
301 <211> LENGTH: 213  
302 <212> TYPE: PRT  
303 <213> ORGANISM: Arabidopsis thaliana  
305 <400> SEQUENCE: 6  
306 Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu  
--> 307    1        5        10        15  
308 Pro Gln Gly Gly Asp Tyr Cys Pro Thr Leu Ala Thr Ser Cys Pro Lys  
--> 309    20        25        30  
310 Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His Pro Ile Tyr  
--> 311    35        40        45  
312 Arg Gly Val Arg Gln Arg Asn Ser Gly Lys Trp Val Ser Glu Val Arg  
--> 313    50        55        60  
314 Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala  
--> 315    65        70        75        80  
316 Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala Leu Arg Gly  
--> 317    85        90        95  
318 Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile  
E--> 319    100        105        110  
320 Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala Glu Ala  
E--> 321    115        120        125  
322 Ala Leu Ala Phe Gln Asp Glu Thr Cys Asp Thr Thr Thr Asn His  
E--> 323    130        135        140  
324 Gly Leu Asp Met Glu Glu Thr Met Val Glu Ala Ile Tyr Thr Pro Glu  
E--> 325    145        150        155        160  
326 Gln Ser Glu Gly Ala Phe Tyr Met Asp Glu Glu Thr Met Phe Gly Met  
E--> 327    165        170        175  
328 Pro Thr Leu Leu Asp Asn Met Ala Glu Gly Met Leu Leu Pro Pro Pro  
E--> 329    180        185        190  
330 Ser Val Gln Trp Asn His Asn Tyr Asp Gly Glu Gly Asp Gly Asp Val  
E--> 331    195        200        205  
332 Ser Leu Trp Ser Tyr  
E--> 333    210  
393 <210> SEQ ID NO: 8  
394 <211> LENGTH: 216  
395 <212> TYPE: PRT  
396 <213> ORGANISM: Arabidopsis thaliana  
398 <400> SEQUENCE: 8  
399 Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu  
E--> 400    1        5        10        15  
401 Ser Pro Val Ser Ser Gly Gly Asp Tyr Ser Pro Lys Leu Ala Thr Ser  
E--> 402    20        25        30  
403 Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His  
E--> 404    35        40        45  
405 Pro Ile Tyr Arg Gly Val Arg Gln Arg Asn Ser Gly Lys Trp Val Cys  
E--> 406    50        55        60  
407 Glu Leu Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/798,579

DATE: 03/22/2004  
TIME: 10:19:03

Input Set : A:\PTO.DA.txt  
Output Set: N:\CRF4\03222004\J798579.raw

Some errors

--> 408 65 70 75 80  
409 Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Ile Ala  
--> 410 85 90 95  
411 Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg  
--> 412 100 105 110  
413 Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Glu Ile Gln Lys Ala Ala  
--> 414 115 120 125  
415 Ala Glu Ala Ala Leu Asn Phe Gln Asp Glu Met Cys His Met Thr Thr  
--> 416 130 135 140  
417 Asp Ala His Gly Leu Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr  
--> 418 145 150 155 160  
419 Thr Pro Glu Gln Ser Gln Asp Ala Phe Tyr Met Asp Glu Glu Ala Met  
--> 420 165 170 175  
421 Leu Gly Met Ser Ser Leu Leu Asp Asn Met Ala Glu Gly Met Leu Leu  
--> 422 180 185 190  
423 Pro Ser Pro Ser Val Gln Trp Asn Tyr Asn Phe Asp Val Glu Gly Asp  
;--> 424 195 200 205  
425 Asp Asp Val Ser Leu Trp Ser Tyr  
;--> 426 210 215  
517 <210> SEQ ID NO: 10  
518 <211> LENGTH: 330  
519 <212> TYPE: PRT  
520 <213> ORGANISM: Arabidopsis thaliana  
v--> 521 <400> SEQUENCE: 10  
522 Met Ala Val Tyr Glu Gln Thr Gly Thr Glu Gln Pro Lys Lys Arg Lys  
;--> 523 1 5 10 15  
524 Ser Arg Ala Arg Ala Gly Gly Leu Thr Val Ala Asp Arg Leu Lys Lys  
E--> 525 20 25 30  
526 Trp Lys Glu Tyr Asn Glu Ile Val Glu Ala Ser Ala Val Lys Glu Gly  
E--> 527 35 40 45  
528 Glu Lys Pro Lys Arg Lys Val Pro Ala Lys Gly Ser Lys Lys Gly Cys  
E--> 529 50 55 60  
530 Met Lys Gly Lys Gly Pro Asp Asn Ser His Cys Ser Phe Arg Gly  
E--> 531 65 70 75 80  
532 Val Arg Gln Arg Ile Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro  
E--> 533 85 90 95  
534 Lys Ile Gly Thr Arg Leu Trp Leu Gly Thr Phe Pro Thr Ala Glu Lys  
E--> 535 100 105 110  
536 Ala Ala Ser Ala Tyr Asp Glu Ala Ala Thr Ala Met Tyr Gly Ser Leu  
E--> 537 115 120 125  
538 Ala Arg Leu Asn Phe Pro Gln Ser Val Gly Ser Glu Phe Thr Ser Thr  
E--> 539 130 135 140  
540 Ser Ser Gln Ser Glu Val Cys Thr Val Glu Asn Lys Ala Val Val Cys  
E--> 541 145 150 155 160  
542 Gly Asp Val Cys Val Lys His Glu Asp Thr Asp Cys Glu Ser Asn Pro  
E--> 543 165 170 175  
544 Phe Ser Gln Ile Leu Asp Val Arg Glu Glu Ser Cys Gly Thr Arg Pro  
E--> 545 180 185 190  
546 Asp Ser Cys Thr Val Gly His Gln Asp Met Asn Ser Ser Leu Asn Tyr

3/22/04

Input Set : A:\PTO.DA.txt  
Output Set: N:\CRF4\03222004\J798579.raw

Some errors

--> 547 195 200 205  
548 Asp Leu Leu Leu Glu Phe Glu Gln Gln Tyr Trp Gly Gln Val Leu Gln  
--> 549 210 215 220  
550 Glu Lys Glu Lys Pro Lys Gln Glu Glu Glu Ile Gln Gln Gln Gln  
--> 551 225 230 235 240  
552 Gln Gln Gln Gln Gln Gln Leu Gln Pro Asp Leu Leu Thr Val Ala  
--> 553 245 250 255  
554 Asp Tyr Gly Trp Pro Trp Ser Asn Asp Ile Val Asn Asp Gln Thr Ser  
--> 555 260 265 270  
556 Trp Asp Pro Asn Glu Cys Phe Asp Ile Asn Glu Leu Leu Gly Asp Leu  
--> 557 275 280 285  
558 Asn Glu Pro Gly Pro His Gln Ser Gin Asp Gln Asn His Val Asn Ser  
;--> 559 290 295 300  
560 Gly Ser Tyr Asp Leu His Pro Leu His Leu Glu Pro His Asp Gly His  
;--> 561 305 310 315 320  
562 Glu Phe Asn Gly Leu Ser Ser Leu Asp Ile  
;--> 563 325 330  
584 <210> SEQ ID NO: 12  
585 <211> LENGTH: 224  
586 <212> TYPE: PRT  
587 <213> ORGANISM: Arabidopsis thaliana  
589 <400> SEQUENCE: 12  
590 Met Asn Pro Phe Tyr Ser Thr Phe Pro Asp Ser Phe Leu Ser Ile Ser  
E--> 591 1 5 10 15  
593 Asp His Arg Ser Pro Val Ser Asp Ser Ser Glu Cys Ser Pro Lys Leu  
E--> 594 20 25 30  
596 Ala Ser Ser Cys Pro Lys Lys Arg Ala Gly Arg Lys Lys Phe Arg Glu  
E--> 597 35 40 45  
599 Thr Arg His Pro Ile Tyr Arg Gly Val Arg Gln Arg Asn Ser Gly Lys  
E--> 600 50 55 60  
602 Trp Val Cys Glu Val Arg Glu Pro Asn Lys Lys Ser Arg Ile Trp Leu  
E--> 603 65 70 75 80  
605 Gly Thr Phe Pro Thr Val Glu Met Ala Ala Arg Ala His Asp Val Ala  
E--> 606 85 90 95  
608 Ala Leu Ala Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser  
E--> 609 100 105 110  
611 Ala Trp Arg Leu Arg Ile Pro Glu Thr Thr Cys Pro Lys Glu Ile Gln  
E--> 612 115 120 125  
614 Lys Ala Ala Ser Glu Ala Ala Met Ala Phe Gln Asn Glu Thr Thr  
E--> 615 130 135 140  
617 Glu Gly Ser Lys Thr Ala Ala Glu Ala Glu Ala Ala Gly Glu Gly  
E--> 618 145 150 155 160  
620 Val Arg Glu Gly Glu Arg Arg Ala Glu Glu Gln Asn Gly Gly Val Phe  
E--> 621 165 170 175  
623 Tyr Met Asp Asp Glu Ala Leu Leu Gly Met Pro Asn Phe Phe Glu Asn  
E--> 624 180 185 190  
626 Met Ala Glu Gly Met Leu Leu Pro Pro Pro Glu Val Gly Trp Asn His  
E--> 627 195 200 205  
629 Asn Asp Phe Asp Gly Val Gly Asp Val Ser Leu Trp Ser Phe Asp Glu

Input Set : A:\PTO.DA.txt  
Output Set: N:\CRF4\03222004\J798579.raw

*C Same errors*

--> 630 210 215 220  
650 <210> SEQ ID NO: 14  
651 <211> LENGTH: 181  
652 <212> TYPE: PRT  
653 <213> ORGANISM: Arabidopsis thaliana  
655 <400> SEQUENCE: 14  
656 Met Glu Asn Asp Asp Ile Thr Val Ala Glu Met Lys Pro Lys Lys Arg  
--> 657 1 5 10 15  
659 Ala Gly Arg Arg Ile Phe Lys Glu Thr Arg His Pro Ile Tyr Arg Gly  
--> 660 20 25 30  
662 Val Arg Arg Arg Asp Gly Asp Lys Trp Val Cys Glu Val Arg Glu Pro  
--> 663 35 40 45  
665 Ile His Gln Arg Arg Val Trp Leu Gly Thr Tyr Pro Thr Ala Asp Met  
--> 666 50 55 60  
668 Ala Ala Arg Ala His Asp Val Ala Val Leu Ala Leu Arg Gly Arg Ser  
--> 669 65 70 75 80  
671 Ala Cys Leu Asn Phe Ser Asp Ser Ala Trp Arg Leu Pro Val Pro Ala  
--> 672 85 90 95  
674 Ser Thr Asp Pro Asp Thr Ile Arg Arg Thr Ala Ala Glu Ala Ala Glu  
--> 675 100 105 110  
677 Met Phe Arg Pro Pro Glu Phe Ser Thr Gly Ile Thr Val Leu Pro Ser  
--> 678 115 120 125  
680 Ala Ser Glu Phe Asp Thr Ser Asp Glu Gly Val Ala Gly Met Met Met  
--> 681 130 135 140  
683 Arg Leu Ala Glu Glu Pro Leu Met Ser Pro Pro Arg Ser Tyr Ile Asp  
E--> 684 145 150 155 160  
686 Met Asn Thr Ser Val Tyr Val Asp Glu Glu Met Cys Tyr Glu Asp Leu  
E--> 687 165 170 175  
689 Ser Leu Trp Ser Tyr  
E--> 690 180  
709 <210> SEQ ID NO: 16  
710 <211> LENGTH: 209  
711 <212> TYPE: PRT  
712 <213> ORGANISM: Arabidopsis thaliana  
714 <400> SEQUENCE: 16  
715 Met Asn Asn Asp Asp Ile Ile Leu Ala Glu Met Arg Pro Lys Lys Arg  
E--> 716 1 5 10 15  
717 Ala Gly Arg Arg Val Phe Lys Glu Thr Arg His Pro Val Tyr Arg Gly  
E--> 718 20 25 30  
720 Ile Arg Arg Arg Asn Gly Asp Lys Trp Val Cys Glu Val Arg Glu Pro  
E--> 721 35 40 45  
723 Thr His Gln Arg Arg Ile Trp Leu Gly Thr Tyr Pro Thr Ala Asp Met  
E--> 724 50 55 60  
726 Ala Ala Arg Ala His Asp Val Ala Val Leu Ala Leu Arg Gly Arg Ser  
E--> 727 65 70 75 80  
729 Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg Leu Pro Val Pro Glu  
E--> 730 85 90 95  
732 Ser Asn Asp Pro Asp Val Ile Arg Arg Val Ala Ala Glu Ala Ala Glu  
E--> 733 100 105 110

Input Set : A:\PTO.DA.txt  
Output Set: N:\CRF4\03222004\J798579.raw

Sample errors

735 Met Phe Arg Pro Val Asp Leu Glu Ser Gly Ile Thr Val Leu Pro Cys  
--> 736 115 120 125  
738 Ala Gly Asp Asp Val Asp Leu Gly Phe Gly Ser Gly Ser Gly  
--> 739 130 135 140  
741 Ser Gly Ser Glu Glu Arg Asn Ser Ser Tyr Gly Phe Gly Asp Tyr  
--> 742 145 150 155 160  
744 Glu Glu Val Ser Thr Thr Met Met Arg Leu Ala Glu Gly Pro Leu Met  
--> 745 165 170 175  
746 Ser Pro Pro Arg Ser Tyr Met Glu Asp Met Thr Pro Thr Asn Val Tyr  
--> 747 180 185 190  
749 Thr Glu Glu Glu Met Cys Tyr Glu Asp Met Ser Leu Trp Ser Tyr Arg  
--> 750 195 200 205  
752 Tyr  
781 <210> SEQ ID NO: 18  
782 <211> LENGTH: 341  
783 <212> TYPE: PRT  
784 <213> ORGANISM: Arabidopsis thaliana  
786 <400> SEQUENCE: 18  
787 Met Pro Ser Glu Ile Val Asp Arg Lys Arg Lys Ser Arg Gly Thr Arg  
--> 788 1 5 10 15  
790 Asp Val Ala Glu Ile Leu Arg Gln Trp Arg Glu Tyr Asn Glu Gln Ile  
--> 791 20 25 30  
793 Glu Ala Glu Ser Cys Ile Asp Gly Gly Pro Lys Ser Ile Arg Lys  
E--> 794 35 40 45  
796 Pro Pro Pro Lys Gly Ser Arg Lys Gly Cys Met Lys Gly Lys Gly  
E--> 797 50 55 60  
799 Pro Glu Asn Gly Ile Cys Asp Tyr Arg Gly Val Arg Gln Arg Arg Trp  
E--> 800 65 70 75 80  
801 Gly Lys Trp Val Ala Glu Ile Arg Glu Pro Asp Gly Ala Arg Leu  
E--> 802 85 90 95  
804 Trp Leu Gly Thr Phe Ser Ser Ser Tyr Glu Ala Ala Leu Ala Tyr Asp  
E--> 805 100 105 110  
807 Glu Ala Ala Lys Ala Ile Tyr Gly Gln Ser Ala Arg Leu Asn Leu Pro  
E--> 808 115 120 125  
810 Glu Ile Thr Asn Arg Ser Ser Ser Thr Ala Ala Thr Ala Thr Val Ser  
E--> 811 130 135 140  
813 Gly Ser Val Thr Ala Phe Ser Asp Glu Ser Glu Val Cys Ala Arg Glu  
E--> 814 145 150 155 160  
816 Asp Thr Asn Ala Ser Ser Gly Phe Gly Gln Val Lys Leu Glu Asp Cys  
E--> 817 165 170 175  
819 Ser Asp Glu Tyr Val Leu Leu Asp Ser Ser Gln Cys Ile Lys Glu Glu  
E--> 820 180 185 190  
822 Leu Lys Gly Lys Glu Glu Val Arg Glu Glu His Asn Leu Ala Val Gly  
E--> 823 195 200 205  
825 Phe Gly Ile Gly Gln Asp Ser Lys Arg Glu Thr Leu Asp Ala Trp Leu  
E--> 826 210 215 220  
828 Met Gly Asn Gly Asn Glu Gln Glu Pro Leu Glu Phe Gly Val Asp Glu  
E--> 829 225 230 235 240  
830 Thr Phe Asp Ile Asn Glu Leu Leu Gly Ile Leu Asn Asp Asn Asn Val

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/798,579

DATE: 03/22/2004  
TIME: 10:19:03

Input Set : A:\PTO.DA.txt  
Output Set: N:\CRF4\03222004\J798579.raw

↙ Same  
errors

--> 831        245        250        255  
833 Ser Gly Gln Glu Thr Met Gln Tyr Gln Val Asp Arg His Pro Asn Phe  
--> 834        260        265        270  
836 Ser Tyr Gln Thr Gln Phe Pro Asn Ser Asn Leu Leu Gly Ser Leu Asn  
--> 837        275        280        285  
839 Pro Met Glu Ile Ala Gln Pro Gly Val Asp Tyr Gly Cys Pro Tyr Val  
;--> 840        290        295        300  
842 Gln Pro Ser Asp Met Glu Asn Tyr Gly Ile Asp Leu Asp His Arg Arg  
;--> 843 305        310        315        320  
845 Phe Asn Asp Leu Asp Ile Gln Asp Leu Asp Phe Gly Gly Asp Lys Asp  
;--> 846        325        330        335  
848 Val His Gly Ser Thr  
;--> 849        340  
870 <210> SEQ ID NO: 20  
871 <211> LENGTH: 206  
872 <212> TYPE: PRT  
873 <213> ORGANISM: Arabidopsis thaliana  
875 <400> SEQUENCE: 20  
876 Met Ser Ser Ile Glu Pro Lys Val Met Met Val Gly Ala Asn Lys Lys  
E--> 877 1        5        10        15  
879 Gln Arg Thr Val Gln Ala Ser Ser Arg Lys Gly Cys Met Arg Gly Lys  
E--> 880 20        25        30  
882 Gly Gly Pro Asp Asn Ala Ser Cys Thr Tyr Lys Gly Val Arg Gln Arg  
E--> 883 35        40        45  
885 Thr Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro Asn Arg Gly Ala  
E--> 886 50        55        60  
888 Arg Leu Trp Leu Gly Thr Phe Asp Thr Ser Arg Glu Ala Ala Leu Ala  
E--> 889 65        70        75        80  
891 Tyr Asp Ser Ala Ala Arg Lys Leu Tyr Gly Pro Glu Ala His Leu Asn  
E--> 892 85        90        95  
894 Leu Pro Glu Ser Leu Arg Ser Tyr Pro Lys Thr Ala Ser Ser Pro Ala  
E--> 895 100        105        110  
897 Ser Gln Thr Thr Pro Ser Ser Asn Thr Gly Gly Lys Ser Ser Ser Asp  
E--> 898 115        120        125  
900 Ser Glu Ser Pro Cys Ser Ser Asn Glu Met Ser Ser Cys Gly Arg Val  
E--> 901 130        135        140  
903 Thr Glu Glu Ile Ser Trp Glu His Ile Asn Val Asp Leu Pro Val Met  
E--> 904 145        150        155        160  
906 Asp Asp Ser Ser Ile Trp Glu Glu Ala Thr Met Ser Leu Gly Phe Pro  
E--> 907 165        170        175  
909 Trp Val His Glu Gly Asp Asn Asp Ile Ser Arg Phe Asp Thr Cys Ile  
E--> 910 180        185        190  
912 Ser Gly Gly Tyr Ser Asn Trp Asp Ser Phe His Ser Pro Leu  
E--> 913 195        200        205  
938 <210> SEQ ID NO: 22  
939 <211> LENGTH: 244  
940 <212> TYPE: PRT  
941 <213> ORGANISM: Arabidopsis thaliana  
943 <400> SEQUENCE: 22

3/22/04

Input Set : A:\PTO.DA.txt  
Output Set: N:\CRF4\03222004\J798579.raw

944 Met Glu Lys Glu Asp Asn Gly Ser Lys Gln Ser Ser Ser Ala Ser Val  
--> 945 1 5 10 15  
947 Val Ser Ser Arg Arg Arg Arg Arg Val Val Glu Pro Val Glu Ala Thr  
--> 948 20 25 30  
950 Leu Gln Arg Trp Glu Glu Gly Leu Ala Arg Ala Arg Arg Val Gln  
--> 951 35 40 45  
953 Ala Lys Gly Ser Lys Lys Gly Cys Met Arg Gly Lys Gly Pro Glu  
--> 954 50 55 60  
956 Asn Pro Val Cys Arg Phe Arg Gly Val Arg Gln Arg Val Trp Gly Lys  
--> 957 65 70 75 80  
959 Trp Val Ala Glu Ile Arg Glu Pro Val Ser His Arg Gly Ala Asn Ser  
--> 960 85 90 95  
962 Ser Arg Ser Lys Arg Leu Trp Leu Gly Thr Phe Ala Thr Ala Ala Glu  
--> 963 100 105 110  
965 Ala Ala Ile Ala Tyr Asp Arg Ala Ala Ser Val Met Tyr Gly Pro Tyr  
--> 966 115 120 125  
968 Ala Arg Leu Asn Phe Pro Glu Asp Leu Gly Gly Arg Lys Lys Asp  
--> 969 130 135 140  
970 Glu Glu Ala Glu Ser Ser Gly Tyr Trp Leu Glu Thr Asn Lys Ala  
--> 971 145 150 155 160  
973 Gly Asn Gly Val Ile Glu Thr Glu Gly Lys Asp Tyr Val Val Tyr  
E--> 974 165 170 175  
976 Asn Glu Asp Ala Ile Glu Leu Gly His Asp Lys Thr Gln Asn Pro Met  
E--> 977 180 185 190  
979 Thr Asp Asn Glu Ile Val Asn Pro Ala Val Lys Ser Glu Glu Gly Tyr  
E--> 980 195 200 205  
982 Ser Tyr Asp Arg Phe Lys Leu Asp Asn Gly Leu Leu Tyr Asn Glu Pro  
E--> 983 210 215 220  
985 Gln Ser Ser Ser Tyr His Gln Gly Gly Phe Asp Ser Tyr Phe Glu  
E--> 986 225 230 235 240  
988 Tyr Phe Arg Phe  
1013 <210> SEQ ID NO: 24  
1014 <211> LENGTH: 277  
1015 <212> TYPE: PRT  
1016 <213> ORGANISM: Arabidopsis thaliana  
1018 <400> SEQUENCE: 24  
1019 Met Glu Lys Ser Ser Ser Met Lys Gln Trp Lys Lys Gly Pro Ala Arg  
E--> 1020 1 5 10 15  
1022 Gly Lys Gly Gly Pro Gln Asn Ala Leu Cys Gln Tyr Arg Gly Val Arg  
E--> 1023 20 25 30  
1025 Gln Arg Thr Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro Lys Lys  
E--> 1026 35 40 45  
1028 Arg Ala Arg Leu Trp Leu Gly Ser Phe Ala Thr Ala Glu Glu Ala Ala  
E--> 1029 50 55 60  
1031 Met Ala Tyr Asp Glu Ala Ala Leu Lys Leu Tyr Gly His Asp Ala Tyr  
E--> 1032 65 70 75 80  
1034 Leu Asn Leu Pro His Leu Gln Arg Asn Thr Arg Pro Ser Leu Ser Asn  
E--> 1035 85 90 95  
1037 Ser Gln Arg Phe Lys Trp Val Pro Ser Arg Lys Phe Ile Ser Met Phe

Same errors

Input Set : A:\PTO.DA.txt  
Output Set: N:\CRF4\03222004\J798579.raw

Some errors

--> 1038        100        105        110  
1040 Pro Ser Cys Gly Met Leu Asn Val Ala Gln Pro Ser Val His Ile  
--> 1041        115        120        125  
1043 Ile Gln Gln Arg Leu Glu Glu Lys Lys Thr Gly Leu Leu Ser Gln  
--> 1044        130        135        140  
1046 Ser Tyr Ser Ser Ser Ser Thr Glu Ser Lys Thr Asn Thr Ser  
--> 1047        145        150        155        160  
1049 Phe Leu Asp Glu Lys Thr Ser Lys Gly Glu Thr Asp Asn Met Phe Glu  
--> 1050        165        170        175  
1052 Gly Gly Asp Gln Lys Lys Pro Glu Ile Asp Leu Thr Glu Phe Leu Gln  
--> 1053        180        185        190  
1054 Gln Leu Gly Ile Leu Lys Asp Glu Asn Glu Ala Glu Pro Ser Glu Val  
--> 1055        195        200        205  
1057 Ala Glu Cys His Ser Pro Pro Pro Trp Asn Glu Gln Glu Thr Gly  
--> 1058        210        215        220  
1060 Ser Pro Phe Arg Thr Glu Asn Phe Ser Trp Asp Thr Leu Ile Glu Met  
--> 1061        225        230        235        240  
1063 Pro Arg Ser Glu Thr Thr Met Gln Phe Asp Ser Ser Asn Phe Gly  
--> 1064        245        250        255  
1066 Ser Tyr Asp Phe Glu Asp Asp Val Ser Phe Pro Ser Ile Trp Asp Tyr  
;--> 1067        260        265        270  
1069 Tyr Gly Ser Leu Asp  
;--> 1070        275  
1096 <210> SEQ ID NO: 26  
1097 <211> LENGTH: 306  
1098 <212> TYPE: PRT  
1099 <213> ORGANISM: Arabidopsis thaliana  
1101 <400> SEQUENCE: 26  
1102 Glu Glu Glu Gln Pro Pro Ala Lys Lys Arg Asn Met Gly Arg Ser Arg  
E--> 1103 1        5        10        15  
1105 Lys Gly Cys Met Lys Gly Lys Gly Pro Glu Asn Ala Thr Cys Thr  
E--> 1106        20        25        30  
1108 Phe Arg Gly Val Arg Gln Arg Thr Trp Gly Lys Trp Val Ala Glu Ile  
E--> 1109        35        40        45  
1110 Arg Glu Pro Asn Arg Gly Thr Arg Leu Trp Leu Gly Thr Phe Asn Thr  
E--> 1111        50        55        60  
1113 Ser Val Glu Ala Ala Met Ala Tyr Asp Glu Ala Ala Lys Lys Leu Tyr  
E--> 1114        65        70        75        80  
1116 Gly His Glu Ala Lys Leu Asn Leu Val His Pro Gln Gln Gln Gln  
E--> 1117        85        90        95  
1119 Val Val Val Asn Arg Asn Leu Ser Phe Ser Gly His Gly Ser Gly Ser  
E--> 1120        100        105        110  
1122 Trp Ala Tyr Asn Lys Lys Leu Asp Met Val His Gly Leu Asp Leu Gly  
E--> 1123        115        120        125  
1125 Leu Gly Gln Ala Ser Cys Ser Arg Gly Ser Cys Ser Glu Arg Ser Ser  
E--> 1126        130        135        140  
1128 Phe Leu Gln Glu Asp Asp His Ser His Asn Arg Cys Ser Ser Ser  
E--> 1129        145        150        155        160  
1131 Ser Gly Ser Asn Leu Cys Trp Leu Leu Pro Lys Gln Ser Asp Ser Gln

Input Set : A:\PTO.DA.txt  
Output Set: N:\CRF4\03222004\J798579.raw

{ Some  
errors }

--> 1132 165 170 175  
1134 Asp Gln Glu Thr Val Asn Ala Thr Thr Ser Tyr Gly Gly Glu Gly Gly  
--> 1135 180 185 190  
1137 Gly Gly Ser Thr Leu Thr Phe Ser Thr Asn Leu Lys Pro Lys Asn Leu  
--> 1138 195 200 205  
1139 Met Ser Gln Asn Tyr Gly Leu Tyr Asn Gly Ala Trp Ser Arg Phe Leu  
--> 1140 210 215 220  
1142 Val Gly Gln Glu Lys Lys Thr Glu His Asp Val Ser Ser Cys Gly  
--> 1143 225 230 235 240  
1145 Ser Ser Asp Asn Lys Glu Ser Met Leu Val Pro Ser Cys Gly Gly Glu  
--> 1146 245 250 255  
1148 Arg Met His Arg Pro Glu Leu Glu Arg Thr Gly Tyr Leu Glu Met  
--> 1149 260 265 270  
1151 Asp Asp Leu Leu Glu Ile Asp Asp Leu Gly Leu Leu Ile Gly Lys Asn  
--> 1152 275 280 285  
1154 Gly Asp Phe Lys Asn Trp Cys Cys Glu Glu Phe Gln His Pro Trp Asn  
--> 1155 290 295 300  
1157 Trp Phe  
1158 305  
1177 <210> SEQ ID NO: 28  
1178 <211> LENGTH: 177  
1179 <212> TYPE: PRT  
1180 <213> ORGANISM: Arabidopsis thaliana  
1182 <400> SEQUENCE: 28  
1183 Met Pro Arg Lys Arg Lys Ser Arg Gly Thr Arg Asp Val Ala Glu Ile  
E--> 1184 1 5 10 15  
1186 Leu Arg Lys Trp Arg Glu Tyr Asn Glu Gln Thr Glu Ala Asp Ser Cys  
E--> 1187 20 25 30  
1189 Ile Asp Gly Gly Ser Lys Pro Ile Arg Lys Ala Pro Pro Lys Arg  
E--> 1190 35 40 45  
1192 Ser Arg Lys Gly Cys Met Lys Gly Lys Gly Pro Glu Asn Gly Ile  
E--> 1193 50 55 60  
1194 Cys Asp Tyr Thr Gly Val Arg Gln Arg Thr Trp Gly Lys Trp Val Ala  
E--> 1195 65 70 75 80  
1197 Glu Ile Arg Glu Pro Gly Arg Gly Ala Lys Leu Trp Leu Gly Thr Phe  
E--> 1198 85 90 95  
1200 Ser Ser Ser Tyr Glu Ala Ala Leu Ala Tyr Asp Glu Ala Ser Lys Ala  
E--> 1201 100 105 110  
1203 Ile Tyr Gly Gln Ser Ala Arg Leu Asn Leu Pro Leu Leu Pro Leu Cys  
E--> 1204 115 120 125  
1206 Gln Ala Arg Leu Leu His Phe Leu Met Asn Leu Lys Phe Val His Val  
E--> 1207 130 135 140  
1209 Arg Ile Gln Met Gln Asp Leu Val Leu Val Arg Ser Leu Thr Ser Arg  
E--> 1210 145 150 155 160  
1212 Ile Ser Lys Met Leu Ser Pro Ile Thr Ala Leu Val Lys Leu Gly Arg  
E--> 1213 165 170 175  
1215 Tyr  
1228 <210> SEQ ID NO: 30  
1229 <211> LENGTH: 18

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/798,579

DATE: 03/22/2004  
TIME: 10:19:03

Input Set : A:\PTO.DA.txt  
Output Set: N:\CRF4\03222004\J798579.raw

1230 <212> TYPE: DNA  
1231 <213> ORGANISM: Artificial Sequence  
1233 <220> FEATURE:  
1234 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
1236 <400> SEQUENCE: 30  
1237 cgaracgtcg tcatcatc 18  
--> 1240 2/1  
--> 1241 1/9

Delete

3/22/04

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<400> 1  
cctgaactag aacagaaaaga gagagaaaact attatttcag caaacccatac caacaaaaaa 60  
gacagagatc ttttagttac cttatccagt ttcttgaaac agagtactt tctgtatca 118  
atg aac tca ttt tct gct ttt gaa atg ttt ggc tcc gat tac gag 166  
Met Asn Ser Phe Ser Ala Phe Ser Glu Met Phe Gly Ser Asp Tyr Glu  
1 8 5 10 15  
tct tcg gtt tcc tca ggc ggt gat tat att ccg acg ctt gcg agc agc 214  
Ser Ser Val Ser Ser Gly Gly Asp Tyr Ile Pro Thr Leu Ala Ser Ser  
20 25 30

~ same error  
Please see  
item # 3 &  
4 on  
= error  
summary  
sheet.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/798,579

DATE: 03/22/2004  
TIME: 10:19:04

Input Set : A:\PTO.DA.txt  
Output Set: N:\CRF4\03222004\J798579.raw

::10 M:270 C: Current Application Number differs, Replaced Current Application No  
..:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
..:29 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
..:32 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
..:35 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
..:38 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
..:41 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
..:44 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
..:47 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
..:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
..:53 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
..:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
..:59 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
..:62 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
..:65 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:68 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:80 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2 ✓

M:332 Repeated in SeqNo=2  
L:116 M:283 W: Missing Blank Line separator, <400> field identifier  
L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 ✓  
L:127 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:130 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:145 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:148 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:154 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:157 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:160 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:163 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:169 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:172 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:184 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:198 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4 ✓

M:332 Repeated in SeqNo=4  
L:258 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5 ✓  
L:261 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:264 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:267 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:273 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5

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VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/798,579

DATE: 03/22/2004  
TIME: 10:19:04

Input Set : A:\PTO.DA.txt  
Output Set: N:\CRF4\03222004\J798579.raw

:276 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
:279 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
:282 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
:285 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
:288 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
:291 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
:294 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
:307 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6 ✓  
I:332 Repeated in SeqNo=6  
J:349 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7 ✓  
J:352 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7 ✓  
J:400 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8 ✓  
I:332 Repeated in SeqNo=8  
J:514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:1432  
I:341 Repeated in SeqNo=9  
J:521 M:283 W: Missing Blank Line separator, <400> field identifier  
J:523 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10 ✓  
M:332 Repeated in SeqNo=10  
L:591 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12  
M:332 Repeated in SeqNo=12  
L:657 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14  
M:332 Repeated in SeqNo=14  
L:716 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16  
M:332 Repeated in SeqNo=16  
L:768 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:18  
M:332 Repeated in SeqNo=18  
L:877 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:20  
M:332 Repeated in SeqNo=20  
L:945 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22  
M:332 Repeated in SeqNo=22  
L:1020 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:24  
M:332 Repeated in SeqNo=24  
L:1103 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:26  
M:332 Repeated in SeqNo=26  
L:1184 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:28  
M:332 Repeated in SeqNo=28  
L:1222 M:283 W: Missing Blank Line separator, <220> field identifier ✓  
L:1240 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:19 SEQ:30  
L:1240 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2 ✓  
M:254 Repeated in SeqNo=30  
L:1241 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2 ✓  
L:1241 M:252 E: No. of Seq. differs, <211> LENGTH:Input:18 Found:20 SEQ:30 ✓

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